

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/562,225
Source: IFWP
Date Processed by STIC: 1/10/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/562,225

TIME: 09:20:13

Input Set : A:\47222154.APP

Output Set: N:\CRF4\01102006\J562225.raw

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3 <110> APPLICANT: HILDEBRAND, DAVID
4   RAO, SURYADEVARA S.
6 <120> TITLE OF INVENTION: SOYBEAN SELECTION SYSTEM BASED ON AEC-RESISTANCE
8 <130> FILE REFERENCE: 47100-222154
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/562,225
C--> 11 <141> CURRENT FILING DATE: 2005-12-23
13 <150> PRIOR APPLICATION NUMBER: PCT/US04/020039
14 <151> PRIOR FILING DATE: 2004-06-23
16 <150> PRIOR APPLICATION NUMBER: 60/483,103
17 <151> PRIOR FILING DATE: 2003-06-30
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn Ver. 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 700
25 <212> TYPE: DNA
26 <213> ORGANISM: Glycine max
28 <220> FEATURE:
29 <221> NAME/KEY: MOD_RES
30 <222> LOCATION: (664)
31 <223> OTHER INFORMATION: a, c, g, t, unknown or other
33 <220> FEATURE:
34 <221> NAME/KEY: MOD_RES
35 <222> LOCATION: (696)
36 <223> OTHER INFORMATION: a, c, g, t, unknown or other
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40 tgttattggt ggtgggacaa ctggtgaagg ccaattaatg agccgggaag agcacataat 120
41 acttattgct catacagtca actgttttgg tgggaaaatt aaggttattg gaaatactgg 180
42 aagcaactcc accagggaag caattcatgc cactgagcag ggttttgctg ttggaatgca 240
43 tgctgccctt cacataaacc cttactatgg caaaacctcc ttggatggta tggttgctca 300
44 ctttcgaagt gtgctttcca tgggaccac aataatctac aatgtgcctg cacggaccgg 360
45 acaagacatt cctccgcatg taattcaaac cttagctgaa agtggttaacc tggctggtgt 420
46 caaggagtgt gtgggaaatg accgaatcaa acagtataca gatgatggaa ttgttgtgtg 480
47 gagtgggaat gatgatcaat gtcgatgatg tagatggggg tatgggggcta ccggagtggg 540
48 atctgttgcg agcaacctgg ttccccggtt aatgcgagaa ctcatgtttg gcggtgtaaa 600
49 ccctactcta aattctaaac tcttgctctt gattgactgg cttttccaca tgccaaaccc 660
W--> 50 catnggtttg aacactgctc ttgctcaact tggggmcatc 700
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 1197
55 <212> TYPE: DNA
56 <213> ORGANISM: Escherichia coli
58 <400> SEQUENCE: 2
59 ccaggcgact gtcttcaata ttacagccgc aactactgac atgacgggtg atggtgttca 60

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60 caattccacg gcgatcgga cccaacgcag tgatcaccag ataatgtgtt gcgatgacag 120
61 tgtcaaaactg gttattcctt taaggggtga gttgttctta aggaaagcat aaaaaaaca 180
62 tgcatacaac aatcagaacg gttctgtctg cttgctttta atgccatacc aaacgtacca 240
63 ttgagacact tgtttgaca gaggatggcc catgttcacg ggaagtattg tcgcgattgt 300
64 tactccgatg gatgaaaaag gtaatgtctg tcgggctagc ttgaaaaaac tgattgatta 360
65 tcatgtcgcc agcgggtactt cggcgatcgt ttctgttggc accactggcg agtccgctac 420
66 cttaaactcat gacgaacatg ctgatgtggt gatgatgacg ctggatctgg ctgatgggcg 480
67 cattccggta attgccggga ccggcgctaa cgctactgcg gaagccatta gcctgacgca 540
68 gcgcttcaat gacagtggta tcgtcggtcg cctgacggta accccttact acaatcgctc 600
69 gtcgcaagaa ggtttgtatc agcatttcaa agccatcgct gagcatactg acctgccgca 660
70 aattctgtat aatgtgccgt cccgtactgg ctgcatctg ctcccggaaa cgggtgggccc 720
71 tctggcgaaa gtaaaaaata ttatcggaat caaagaggca acagggaact taacgcgtgt 780
72 aaaccagatc aaagagctgg ttccagatga ttttgttctg ctgagcggcg atgatgcgag 840
73 cgcgctggac ttatgcaat tgggcggtca tgggggttatt tccgttacga ctaacgtcgc 900
74 agcgcgtgat atggcccaga tgtgcaaaact ggcagcagaa gaacattttg ccgaggcgacg 960
75 cgttattaat cagcgtctga tgccattaca caacaaacta tttgtcgaac ccaatccaat 1020
76 cccggtgaaa tgggcatgta aggaactggg tcttgtggcg accgatacgc tgcgcctgcc 1080
77 aatgacacca atcaccgaca gtggctcgtga gacggtcaga gcggcgctta agcatgccgg 1140
78 tttgctgtaa agtttaggga gatttgatgg cttactctgt tcaaaagtcg cgctgg 1197

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81 <210> SEQ ID NO: 3

82 <211> LENGTH: 292

83 <212> TYPE: PRT

84 <213> ORGANISM: Escherichia coli

86 <400> SEQUENCE: 3

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88 1 5 10 15
90 Gly Asn Val Cys Arg Ala Ser Leu Lys Lys Leu Ile Asp Tyr His Val
91 20 25 30
93 Ala Ser Gly Thr Ser Ala Ile Val Ser Val Gly Thr Thr Gly Glu Ser
94 35 40 45
96 Ala Thr Leu Asn His Asp Glu His Ala Asp Val Val Met Met Thr Leu
97 50 55 60
99 Asp Leu Ala Asp Gly Arg Ile Pro Val Ile Ala Gly Thr Gly Ala Asn
100 65 70 75 80
102 Ala Thr Ala Glu Ala Ile Ser Leu Thr Gln Arg Phe Asn Asp Ser Gly
103 85 90 95
105 Ile Val Gly Cys Leu Thr Val Thr Pro Tyr Tyr Asn Arg Pro Ser Gln
106 100 105 110
108 Glu Gly Leu Tyr Gln His Phe Lys Ala Ile Ala Glu His Thr Asp Leu
109 115 120 125
111 Pro Gln Ile Leu Tyr Asn Val Pro Ser Arg Thr Gly Cys Asp Leu Leu
112 130 135 140
114 Pro Glu Thr Val Gly Arg Leu Ala Lys Val Lys Asn Ile Ile Gly Ile
115 145 150 155 160
117 Lys Glu Ala Thr Gly Asn Leu Thr Arg Val Asn Gln Ile Lys Glu Leu
118 165 170 175
120 Val Ser Asp Asp Phe Val Leu Leu Ser Gly Asp Asp Ala Ser Ala Leu
121 180 185 190
123 Asp Phe Met Gln Leu Gly Gly His Gly Val Ile Ser Val Thr Thr Asn

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124          195          200          205
126 Val Ala Ala Arg Asp Met Ala Gln Met Cys Lys Leu Ala Ala Glu Glu
127      210          215          220
129 His Phe Ala Glu Ala Arg Val Ile Asn Gln Arg Leu Met Pro Leu His
130 225          230          235          240
132 Asn Lys Leu Phe Val Glu Pro Asn Pro Ile Pro Val Lys Trp Ala Cys
133          245          250          255
135 Lys Glu Leu Gly Leu Val Ala Thr Asp Thr Leu Arg Leu Pro Met Thr
136          260          265          270
138 Pro Ile Thr Asp Ser Gly Arg Glu Thr Val Arg Ala Ala Leu Lys His
139      275          280          285
141 Ala Gly Leu Leu
142      290
145 <210> SEQ ID NO: 4
146 <211> LENGTH: 332
147 <212> TYPE: PRT
148 <213> ORGANISM: Glycine max
150 <400> SEQUENCE: 4
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152 1          5          10          15
154 Arg Ser Phe Glu Leu Lys Asn Arg Thr Ser Pro Glu Asp Ile Lys Ala
155      20          25          30
157 Leu Arg Leu Ile Thr Ala Ile Lys Thr Pro Tyr Leu Pro Asp Gly Arg
158      35          40          45
160 Phe Asp Leu Glu Ala Tyr Asp Asp Leu Val Asn Met Gln Ile Gly Gln
161      50          55          60
163 Gly Ala Glu Gly Val Ile Val Gly Gly Thr Thr Gly Glu Gly Gln Leu
164 65          70          75          80
166 Met Ser Trp Glu Glu His Ile Ile Leu Ile Ala His Thr Val Asn Cys
167      85          90          95
169 Phe Gly Gly Lys Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr
170      100          105          110
172 Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Val Gly Met His
173      115          120          125
175 Ala Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Leu Asp Gly
176      130          135          140
178 Met Val Ala His Phe Arg Ser Val Leu Ser Met Gly Pro Thr Ile Ile
179 145          150          155          160
181 Tyr Asn Val Pro Ala Arg Thr Gly Gln Asp Ile Pro Pro His Val Ile
182      165          170          175
184 Gln Thr Leu Ala Glu Ser Val Asn Leu Ala Gly Val Lys Glu Cys Val
185      180          185          190
187 Gly Asn Asp Arg Ile Lys Gln Tyr Thr Asp Asp Gly Ile Val Val Trp
188      195          200          205
190 Ser Gly Asn Asp Asp Gln Cys His Asp Ala Arg Trp Gly Tyr Gly Ala
191      210          215          220
193 Thr Gly Val Val Ser Val Ala Ser Asn Leu Val Pro Gly Leu Met Arg
194 225          230          235          240
196 Glu Leu Met Phe Gly Gly Val Asn Pro Thr Leu Asn Ser Lys Leu Leu

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```

197          245          250          255
199 Pro Leu Ile Asp Trp Leu Phe His Met Pro Asn Pro Ile Gly Leu Asn
200          260          265          270
202 Thr Ala Leu Ala Gln Leu Gly Val Ile Arg Pro Val Phe Arg Leu Pro
203          275          280          285
205 Phe Val Pro Leu Pro Val Asp Lys Arg Ile Glu Phe Ala Asn Leu Val
206          290          295          300
208 Lys Glu Ile Gly Arg Glu His Phe Val Gly Asn Lys Val Val Glu Val
209 305          310          315          320
211 Leu Asp Asp Asp Asp Phe Phe Leu Val Ser Arg Tyr
212          325          330
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 215
217 <212> TYPE: PRT
218 <213> ORGANISM: Glycine max
220 <400> SEQUENCE: 5
221 Tyr Asp Asp Leu Val Asn Met Gln Ile Gly Gln Gly Ala Glu Gly Val
222 1          5          10          15
224 Ile Val Gly Gly Thr Thr Gly Glu Gly Gln Leu Met Ser Arg Glu Glu
225          20          25          30
227 His Ile Ile Leu Ile Ala His Thr Val Asn Cys Phe Gly Gly Lys Ile
228          35          40          45
230 Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr Arg Glu Ala Ile His
231          50          55          60
233 Ala Thr Glu Gln Gly Phe Ala Val Gly Met His Ala Ala Leu His Ile
234 65          70          75          80
236 Asn Pro Tyr Tyr Gly Lys Thr Ser Leu Asp Gly Met Val Ala His Phe
237          85          90          95
239 Arg Ser Val Leu Ser Met Gly Pro Thr Ile Ile Tyr Asn Val Pro Ala
240          100          105          110
242 Arg Thr Gly Gln Asp Ile Pro Pro His Val Ile Gln Thr Leu Ala Glu
243          115          120          125
245 Ser Val Asn Leu Ala Gly Val Lys Glu Cys Val Gly Asn Asp Arg Ile
246          130          135          140
248 Lys Gln Tyr Thr Asp Asp Gly Ile Val Val Trp Ser Gly Asn Asp Asp
249 145          150          155          160
251 Gln Cys His Asp Ala Arg Trp Gly Tyr Gly Ala Thr Gly Val Val Ser
252          165          170          175
254 Val Ala Ser Asn Leu Val Pro Gly Leu Met Arg Glu Leu Met Phe Gly
255          180          185          190
257 Gly Val Asn Pro Thr Leu Asn Ser Lys Leu Leu Pro Leu Ile Asp Trp
258          195          200          205
260 Leu Phe His Met Pro Asn Pro
261          210          215
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 7
266 <212> TYPE: PRT
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:

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270 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
271 consensus sequence
273 <400> SEQUENCE: 6
274 Met Ser Trp Asp Glu His Ile
275 1 5

RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : A:\47222154.APP

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 664,696

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/562,225

DATE: 01/10/2006

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Input Set : A:\47222154.APP

Output Set: N:\CRF4\01102006\J562225.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:660